

Supplemental Table 2. Top network and GO processes

#	Network	GO processes	Total	Seed	p-Value	zScore	gScore
			nodes	nodes			
1	Transthyretin, E2F1, TCF7L2 (TCF4), Myelin basic protein, GLNA	response to hormone (49.2%; 2.611e-18), response to endogenous stimulus (57.6%; 3.004e-18), regulation of population proliferation (55.9%; 2.906e-17), regulation of multicellular organismal process (64.4%; 2.641e-16), animal organ development (71.2%; 4.179e-16)	67	28	1.89E-94	286.31	286.31
2	HBB, HBZ, MSP receptor (RON), SHP-2, Epo	cytokine-mediated signaling pathway (42.9%; 1.198e-19), cellular response to cytokine stimulus (48.2%; 8.224e-18), immune system process (67.9%; 2.234e-17), regulation of cell population proliferation (57.1%; 3.713e-17), animal organ development (73.2%; 1.831e-16)	58	27	1.34E-92	297.09	297.09
3	BETA-IG-H3, NCOA3 (pCIP/SRC3), Estradiol cytoplasm, Hyaluronic acid	regulated exocytosis (50.0%; 1.276e-10), exocytosis (50.0%; 4.467e-10), secretion by cell (50.0%; 4.347e-09), export from cell (50.0%; 7.552e-09), secretion (50.0%; 1.741e-08)	24	16	1.32E-57	271.32	271.32

	extracellular region, ESR1 (nuclear)							
4	SERPINA3 (ACT), Oncostatin M, BMP7, IL-6, Thrombopoietin	cellular response to cytokine stimulus (62.1%; 1.683e-28), cytokine-mediated signaling pathway (51.7%; 2.578e-27), response to cytokine (62.1%; 1.355e-26), regulation of cell population proliferation (63.8%; 5.613e-22), cellular response to interleukin-6 (22.4%; 3.172e-21)	60	16	1.97E-49	173	173	
5	LRG, G-CSF, STAT3, PU.1, STAT5	cellular response to interleukin-6 (30.0%; 3.141e-11), response to interleukin-6 (30.0%; 6.312e-11), interleukin-6- mediated signaling pathway (25.0%; 9.427e-11), receptor signaling pathway via JAK-STAT (25.0%; 1.348e-09), receptor signaling pathway via STAT (25.0%; 1.468e-09)	20	12	2.15E-42	222.91	222.91	
6	Fibrinogen beta, Fibrinogen gamma, Plasma kallikrein, Thrombin, Coagulation factor XII	regulation of blood coagulation (46.2%; 2.424e-32), regulation of hemostasis (46.2%; 2.876e-32), regulation of coagulation (46.2%; 6.603e-32), blood coagulation (56.4%; 8.407e-29), coagulation (56.4%; 9.839e-29)	44	11	8.94E-34	139.31	139.31	

7	c-Fos, BAD, p70 S6 kinase1, C5, H-Ficolin	complement activation (40.9%; 7.569e-26), regulation of complement activation (34.1%; 7.885e-24), activation of immune response (52.3%; 1.046e-23), response to stress (90.9%; 2.262e-22), regulation of humoral immune response (34.1%; 3.533e-22)	58	10	4.90E-29	110.95	110.95
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